replacement paragraphs pursuant to 37 C.F.R. §1.121(b), as well as rewritten, added, and/or cancelled claims pursuant to 37 C.F.R. §1.121 (c)(1)(ii) is attached as Appendix I.

Please substitute the paragraph beginning on page 34, line 16 with the following paragraph:

A5

The MS-Fit sequence database located in the Protein Prospector program was used for protein identification by entering the peptide masses generated by tryptic digestion. The program is available on the Internet at the Internet World Wide Web site of the Protein Prospector at the University of California-San Francisco. Subsequently, other relevant parameters such as protein species, molecular weight and pI range are also entered in order to narrow down the search. In the illustrative examples of the present invention, Homo sapiens was chosen as the species. Since these proteins were obtained from HPLC, no isoelectric point (pI) information was available. Thus, the pI range was set between 3 and 10. The range of molecular weight values for each search was determined by MALDI-TOF or ESI-TOF analysis. The tolerance for the search of peptides against the database was set at 2 Da for MALDI-MS spectra and 0.5 Da for QIT-reTOF-MS spectra.

Please insert the attached sequence listing as new pages 43-45.

IN THE CLAIMS:

A clean version of the rewritten, added and/or cancelled claims with instructions for entry pursuant to 37 C.F.R. § 1.121(c)(1)(i) is included beginning on page two of this communication. A marked-up version of the rewritten, added, and/or cancelled claims pursuant to 37 C.F.R. § 1.121(c)(1)(ii) is attached as Appendix I. A clean version of the entire set of pending claims pursuant to 37 C.F.R. § 1.121(c)(3) is attached at Appendix II.

Please cancel Claims 7 and 25.

Please substitute the following Claims for the previously pending Claims:

A1 sub b1

1. (Once Amended) A method, comprising:

a) providing:

i) a first sample comprising a plurality of proteins;

ii) a second sample comprising a plurality of proteins;

iii) a separating apparatus, wherein said separating apparatus separates proteins based on a physical property;

iv) a mass spectroscopy apparatus; and

b) treating said first and second samples with said separating apparatus to produce a first separated protein sample and a second separated protein sample, wherein said first and second separated protein samples are collected from said separating apparatus in a plurality of fractions, each of said fractions defined by a physical property; and

c) analyzing said plurality of fractions from each of said first and second separated protein samples with said mass spectroscopy apparatus to produce a protein profile map for each of said first and second samples, wherein said protein profile maps display protein abundance and mass of said first protein sample and said second protein sample, and wherein said protein profile maps displays each protein as a separate band corresponding to said mass of said first protein sample and said second protein sample, and wherein the intensity of said band corresponds to said protein abundance of said first protein sample and said second protein sample.

A1 Cont'd

A2 SUB B1

8. (Once Amended) The method of Claim 1, wherein said bands are bands of different colors.

A3 SUB B1

15. (Once Amended) The method of Claim 14, wherein said buffer comprises a compound of the formula n-octyl C_6-C_{12} glycopyranoside.

A4 SUB B1

23. (Once Amended) A method, comprising:

a) providing:

i) a cell lysate derived from a cell of unknown type, said cell lysate comprising a plurality of proteins;

ii) a first protein profile map generated by the method of Claim 1;

iii) a separating apparatus, wherein said separating apparatus separates

Appendix II

Pending Claims

1. A method, comprising:

a) providing:

i) a first sample comprising a plurality of proteins;

ii) a second sample comprising a plurality of proteins;

iii) a separating apparatus, wherein said separating apparatus separates proteins based on a physical property;

iv) a mass spectroscopy apparatus; and

b) treating said first and second samples with said separating apparatus to produce a first separated protein sample and a second separated protein sample, wherein said first and second separated protein samples are collected from said separating apparatus in a plurality of fractions, each of said fractions defined by a physical property; and

c) analyzing said plurality of fractions from each of said first and second separated protein samples with said mass spectroscopy apparatus to produce a protein profile map for each of said first and second samples, wherein said protein profile maps display protein abundance and mass of said first protein sample and said second protein sample, and wherein said protein profile maps displays each protein as a separate band corresponding to said mass of said first protein sample and said second protein sample, and wherein the intensity of said band corresponds to said protein abundance of said first protein sample and said second protein sample.

2. The method of Claim 1, further comprising an automated sample handling device operably linked to said separating apparatus and said mass spectroscopy apparatus, wherein said sample handling device transfers said first and second samples to said separating apparatus, and wherein said sample handling device transfers said first and second separated protein samples from said separating apparatus to said mass spectroscopy apparatus.

3. The method of Claim 2, further comprising a centralized control network operably

linked to said automated sample handling device, said separating apparatus, and said mass spectroscopy apparatus, wherein said centralized control network controls the operations of said automated sample handling device, said separating apparatus, and said mass spectroscopy apparatus.

4. The method of Claim 3, wherein said centralized control network comprises computer memory and a computer processor.

5. The method of Claim 1, wherein said first sample comprises a cell lysate from a first cell type and said second sample comprises a cell lysate from second cell type.

6. The method of Claim 5, wherein said first cell type is a cancerous cell type and said second cell type is a non-cancerous cell type.

8. The method of Claim 1, wherein said bands are bands of different colors.

9. The method of Claim 1, wherein said protein abundance and mass are indicative of the cell type of said protein sample.

10. The method of Claim 1, further comprising the step of d) determining the identity of individual bands on said protein profile map.

11. The method of Claim 6, further comprising the step of treating said first sample with an external agent prior to treating said first and second samples with said separating apparatus.

12. The method of Claim 11, wherein said external agent comprises estradiol.

13. The method of Claim 2, wherein said automated sample handling device comprises a switchable, multi-channel valve.

14. The method of Claim 1, wherein said first and second samples further comprise a buffer, wherein said plurality of proteins are solubilized in said buffer and wherein said buffer is compatible with said separating apparatus and said mass spectroscopy apparatus.

15. The method of Claim 14, wherein said buffer comprises a compound of the formula n-octyl C_6-C_{12} glycopyranoside.

16. The method of Claim 15, wherein said compound of the formula n-octyl C_6-C_{12} glycopyranoside is selected from n-octyl ß-D-glucopyranoside and n-octyl ß-D-galactopyranoside.

17. The method of Claim 1, wherein said separating apparatus comprises a liquid phase separating apparatus.

18. The method of Claim 17, wherein said liquid phase separating apparatus comprises a reverse phase HPLC separating apparatus.

19. The method of Claim 18, wherein said reverse phase HPLC comprises non-porous reverse phase HPLC.

20. The method of Claim 1, wherein prior to said analyzing said first and second separated protein samples by mass spectroscopy, said first and second samples are divided into first and second portions and wherein said second portions are subjected to enzymatic digestion.

21. The method of Claim 1, wherein said analyzing said first and second separated protein samples by mass spectrometry comprises analyzing said samples by ESI oa TOF/MS.

22. The method of Claim 1, wherein said analyzing said first and second separated protein samples by mass spectrometry comprises analyzing said samples by a technique selected from the group consisting of ion trap mass spectrometry, ion trap/time-of-flight mass spectrometry, quadrupole and triple quadrupole mass spectrometry, Fourier Transform (ICR)

mass spectrometry, and magnetic sector mass spectrometry.

23. A method, comprising:

a) providing:

i) a cell lysate derived from a cell of unknown type, said cell lysate comprising a plurality of proteins;

ii) a first protein profile map generated by the method of Claim 1;

iii) a separating apparatus, wherein said separating apparatus separates proteins based on a physical property; and

iv) a mass spectroscopy apparatus; and

b) treating said cell lysate with said separating apparatus to produce a separated protein sample; wherein said separated protein sample is collected from said separating apparatus in a plurality of fractions, each of said fractions defined by a physical property;

c) analyzing said plurality of fractions from said separated protein sample with said mass spectroscopy apparatus to produce a second protein profile map, wherein said second protein profile maps displays each protein as a separate band corresponding to said mass of said first protein sample and said second protein sample, and wherein the intensity of said band corresponds to said protein abundance of said first protein sample and said second protein sample; and

d) comparing said first protein profile map and said second protein profile map.

24. The method of Claim 23, wherein said first protein profile map displays protein abundance and mass from cell lysates of several known cell types and said second protein profile map displays protein abundance and mass from said cell lysate of unknown type.

26. The method of Claim 23, wherein said bands are bands of different colors.

27. The method of Claim 24, wherein said protein abundance and mass are indicative of a cell identity.

28. A system comprising:

a) a non-porous reverse phase HPLC separating apparatus;

b) an automated sample handling apparatus configured to receive separated proteins from said reverse phase HPLC separating apparatus;

c) a mass spectroscopy apparatus configured to receive proteins from said automated sample handling apparatus;

d) a processor configured to produce a data representation of a protein profile map of separated proteins analyzed by said mass spectroscopy apparatus, wherein said protein profile map displays protein abundance and mass of a separated protein sample; and

e) a display apparatus that displays said protein profile map.

29. The system of Claim 28, wherein said protein profile map displays protein abundance as bands of varying intensity.

30. The system of Claim 29, wherein said protein abundance is expressed as bands of different colors.

31. The system of Claim 28, wherein said protein abundance and mass are indicative of a cell type of said protein sample.

32. The system of Claim 28, wherein said processor is configured to determine the identity of individual bands on said protein profile map.

33. The system of Claim 28, wherein said automated sample handling device comprises a switchable, multi-channel valve.

34. The system of Claim 28, wherein said mass spectrometry apparatus comprises a ESI oa TOF/MS apparatus.